QTL analysis of seed germination and pre-emergence growth at extreme temperatures in Medicago truncatula

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Résumé en anglais	Enhancing the knowledge on the genetic basis of germination and heterotrophic growth at extreme temperatures is of major importance for improving crop establishment. A quantitative trait loci (QTL) analysis was carried out at sub- and supra-optimal temperatures at these early stages in the model Legume Medicago truncatula. On the basis of an ecophysiological model framework, two populations of recombinant inbred lines were chosen for the contrasting behaviours of parental lines: LR5 at suboptimal temperatures (5 or 10C) and LR4 at a supraoptimal temperature (20C). Seed masses were measured in all lines. For LR5, germination rates and hypocotyl growth were measured by hand, whereas for LR4, imbibition and germination rates as well as early embryonic axis growth were measured using an automated image capture and analysis device. QTLs were found for all traits. The phenotyping framework we defined for measuring variables, distinguished stages and enabled identification of distinct QTLs for seed mass (chromosomes 1, 5, 7 and 8), imbibition (chromosome 4), germination (chromosomes 3, 5, 7 and 8) and heterotrophic growth (chromosomes 1, 2, 3 and 8). The three QTL identified for hypocotyl length at suboptimal temperature explained the largest part of the phenotypic variation (60% together). One digenic interaction was found for hypocotyl width at sub-optimal temperature and the loci involved were linked to additive QTLs for hypocotyl elongation at low temperature. Together with working on a model plant, this approach facilitated the identification of genes specific to each stage that could provide reliable markers for assisting selection and improving crop establishment. With this aim in view, an initial set of putative candidate genes was identified in the light of the role of abscissic acid/gibberellin balance in regulating germination at high temperatures (e.g. ABI4, ABI5), the molecular cascade in response to cold stress (e.g. CBF1, ICE1) and hypotheses on changes in cell elongation (e.g. GASA1, AtEXPA11) with changes in temperatures based on studies at the whole plant scale.
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